

Statement, PTO Form 1449, statutory fee of \$180.00 under 37 C.F.R. 1.17(p), a Mark-Up version of the amendments pursuant to 37 C.F.R. 1.121, an Examiner's Courtesy Copy of the claims pending upon entry of this amendment, an Amendment Transmittal, and a check for \$54.00 (additional claims fee). The time set for this response is January 22, 2002.

Should the United States Patent and Trademark Office determine that any other fee is due or that any refund is owed for this application, the Commissioner is hereby authorized and requested to charge the required fee(s) and/or credit the refund(s) owed to our Deposit Account No. 04-0100.

In response to the Official Action dated October 22, 2002, please amend the above-identified application as follows:

IN THE SPECIFICATION:

For amendments to the specification pursuant to 37 C.F.R. 1.121 see the accompanying "marked up" version pursuant to 1.121.

Please amend the paragraph on page 5 lines 11-17 in the "Brief Description of the Drawings" section of the specification to read as follows:

B¹ Figure 2 depicts the DNA sequence of the C2/4GnT (SEQ ID NO:1; accession #

AF038650) gene and the predicted amino acid sequence of C2/4GnT (SEQ ID NO:2).

31
The amino acid sequence is shown in single letter code. The hydrophobic segment representing the putative transmembrane domain is double-underlined. Two consensus motifs for N-glycosylation are indicated by *asterisks*. The location of the primers used for preparation of the expression constructs are indicated by *single underlining*. A potential polyadenylation signal is indicated in *boldface underlined type*.

Please amend the paragraph on page 5 lines 18-24 in the "Brief Description of the Drawings" section of the specification to read as follows:

32
Figure 3 is an illustration of a sequence comparison between human C2GnT (SEQ ID NO:11; accession # M97347), human C2/4GnT (SEQ ID NO:2; accession # AF038650), and human I-GnT (SEQ ID NO:12; accession # Z19550). Introduced gaps are shown as *hyphens*, and aligned identical residues are *boxed* (*black* for all sequences, and *grey* for two sequences). The putative transmembrane domains are *underlined* with a *single line*. The positions of conserved cysteines are indicated by *asterisks*. One conserved N-glycosylation site is indicated by an *open circle*.
